

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 12:41:56 ; Search time 31.5636 Seconds
(without alignments)
3204.847 Million cell updates/sec

Title: US-10-080-839-7
Perfect score: 2071
Sequence: 1 MSAKGIDYDKLIVRFGSSKI.....KLSFDFQKLAAALEHHHHHH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaphage:*
17: sp_archaea:*

SEQ ID NO: 7

Search Summary

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1872	90.4	475	11	Q9DC65	Q9dc65 mus musculu
2	1872	90.4	481	11	Q99J58	Q99j58 mus musculu
3	1537	74.2	305	11	O70184	O70184 cavia porce
4	1324.5	64.0	420	5	Q9U4Y0	Q9u4y0 drosophila
5	1324.5	64.0	430	5	Q9U4Y1	Q9u4y1 drosophila
6	1320.5	63.8	430	5	Q9VHG2	Q9vhg2 drosophila
7	1269.5	61.3	402	10	Q9SR15	Q9sr15 arabidopsis
8	1001.5	48.4	632	5	Q8IDW3	Q8idw3 plasmodium
9	980	47.3	324	5	Q9U1R2	Q9ulr2 caenorhabdi
10	926	44.7	385	5	Q8SQY5	Q8sqy5 encephalito
11	756.5	36.5	490	5	Q9U1F5	Q9ulf5 leishmania
12	682	32.9	136	6	Q95295	Q95295 sus scrofa
13	294	14.2	157	5	Q9U533	Q9u533 trypanosoma
14	293	14.1	111	5	Q95YL8	Q95yl8 encephalito
15	286	13.8	109	4	Q9UDI5	Q9udi5 homo sapien
16	283.5	13.7	136	6	Q9TS88	Q9ts88 bos taurus
17	247.5	12.0	513	17	Q9HN83	Q9hn83 halobacteri
18	211.5	10.2	341	16	Q8E2J5	Q8e2j5 streptococc
19	211.5	10.2	341	16	Q8DWP7	Q8dwp7 streptococc
20	191	9.2	324	17	Q8TXZ2	Q8txz2 methanopyru
21	188	9.1	364	17	Q9YA64	Q9ya64 aeropyrum p
22	181.5	8.8	331	17	Q979Z1	Q979z1 thermoplasm
23	181	8.7	340	16	Q8DRR1	Q8drr1 streptococc
24	171.5	8.3	351	10	P93018	P93018 arabidopsis
25	171.5	8.3	385	10	Q8S9J2	Q8s9j2 arabidopsis
26	168.5	8.1	895	10	Q9SGN2	Q9sgn2 arabidopsis
27	167	8.1	351	16	Q9RVD6	Q9rvd6 deinococcus
28	158.5	7.7	375	17	Q9V027	Q9v027 pyrococcus
29	156	7.5	372	17	Q8ZYT7	Q8zyt7 pyrobaculum
30	153.5	7.4	317	17	Q8TSI1	Q8tsi1 methanosarc
31	152.5	7.4	682	5	Q9N9B8	Q9n9b8 leishmania
32	152	7.3	317	17	Q8PVK0	Q8pvk0 methanosarc
33	150	7.2	528	11	Q8C183	Q8c183 mus musculu
34	149.5	7.2	327	17	Q9HN62	Q9hn62 halobacteri
35	149.5	7.2	408	10	P93363	P93363 nicotiana t
36	148	7.1	316	17	Q8ZW77	Q8zw77 pyrobaculum
37	147.5	7.1	344	16	Q8KGF5	Q8kgf5 chlorobium
38	147	7.1	528	11	Q91WQ3	Q91wq3 mus musculu
39	146	7.0	375	17	O58739	O58739 pyrococcus
40	145	7.0	332	17	Q9HKT3	Q9hkt3 thermoplasm
41	145	7.0	337	16	Q8Z0Y0	Q8z0y0 salmonella
42	144	7.0	525	5	Q9VV60	Q9vv60 drosophila
43	144	7.0	528	11	Q8BVT2	Q8bvt2 mus musculu
44	142.5	6.9	375	17	Q8U2H3	Q8u2h3 pyrococcus
45	141.5	6.8	363	16	Q8G6N8	Q8g6n8 bifidobacte

ALIGNMENTS

RESULT 1
Q9DC65

OM protein - protein search, using sw model

Run on: February 20, 2004, 12:38:16 ; Search time 38.1818 Seconds
(without alignments)
1629.593 Million cell updates/sec

Title: US-10-080-839-7
Perfect score: 2071
Sequence: 1 MSAKGIDYDKLIVRFGSSKI.....KLSFDFQKLAAALEHHHHHH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Applicants

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2071	100.0	392	22	AAB47618	Human inactive Trp
2	2071	100.0	392	23	AAG79544	His6-tagged TrpRS
3	2071	100.0	392	23	AAE13494	Human inactive try
4	2066	99.8	415	22	AAB47617	Human supermini Tr
5	2066	99.8	415	23	AAG79548	His6-tagged TrpRS
6	2066	99.8	415	23	AAE13493	Human supermini tr
7	2066	99.8	437	22	AAB47616	Human mini TrpRS.
8	2066	99.8	437	23	AAG79547	His6-tagged mini-T
9	2066	99.8	437	23	AAE13492	Human mini tryptop
10	2066	99.8	484	22	AAB47615	Human full-length
11	2066	99.8	484	23	AAG79546	Full length human
12	2066	99.8	484	23	AAE13491	Human tryptophanyl
13	1988	96.0	378	23	AAG79541	TrpRS T2 polypepti
14	1988	96.0	401	23	AAG79549	TrpRS T1 polypepti
15	1973	95.3	378	24	AAG79953	T2-TrpRS. Homo sa
16	1973	95.3	475	21	AAB58220	Lung cancer associ
17	1968	95.0	471	20	AAV05372	Human HCMV inducib
18	1320.5	63.8	430	22	ABB64621	Drosophila melanog
19	1320.5	63.8	430	22	ABB67203	Drosophila melanog
20	1272.5	61.4	402	21	AAG23698	Arabidopsis thalia
21	1272.5	61.4	426	21	AAG23697	Arabidopsis thalia
22	1195.5	57.7	424	22	AAB66931	Tryptophanyl-tRNA
23	1177.5	56.9	424	23	ABP73795	Candida albicans e
24	1119.5	54.1	433	24	ABJ26487	Aspergillus fumiga
25	968	46.7	292	21	AAG23699	Arabidopsis thalia
26	831	40.1	173	21	AAB58517	Lung cancer associ
27	786.5	38.0	385	22	AAB96409	Putative P. abyssi
28	409	19.7	179	24	ABJ25887	Aspergillus fumiga
29	211.5	10.2	341	23	ABP26964	Streptococcus poly
30	200	9.7	85	23	AAE13515	Human tryptophanyl
31	191	9.2	39	24	AAG79951	T2-TrpRS partial s
32	185.5	9.0	341	19	AAW56423	Tryptophanyl tRNA
33	185.5	9.0	341	22	AAU37851	Streptococcus pneu
34	185.5	9.0	341	24	ABU02760	S. pneumoniae type
35	183	8.8	341	23	ABP26965	Streptococcus poly
36	174.5	8.4	341	23	ABB53366	Lactococcus lactis
37	173	8.4	372	22	AAB47614	Human mini TyrRS m
38	173	8.4	372	23	AAE13490	Human mini tyrosyl
39	171.5	8.3	372	22	AAB47612	Human mini TyrRS.
40	171.5	8.3	372	23	AAE13488	Human mini tyrosyl
41	169.5	8.2	409	20	AAW94248	C. albicans tyrosy
42	169.5	8.2	409	23	ABP73498	Candida albicans e
43	167.5	8.1	409	20	AAW94247	C. albicans tyrosy
44	159.5	7.7	379	20	AAV37623	Protein involved i
45	158.5	7.7	378	22	AAB96600	Putative P. abyssi

ALIGNMENTS

OM protein - protein search, using sw model

Run on: February 20, 2004, 12:43:21 ; Search time 15.2727 Seconds
 (without alignments)
 1085.979 Million cell updates/sec

Title: US-10-080-839-7
 Perfect score: 2071
 Sequence: 1 MSAKGIDYDKLIVRFGSSKI.....KLSFDFQKLAAALEHHHHHH 392

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1195.5	57.7	424	3	US-08-876-885-26	Sequence 26, Appl
2	195	9.4	338	4	US-09-328-352-4201	Sequence 4201, Ap
3	193	9.3	348	4	US-09-107-532A-5765	Sequence 5765, Ap
4	185.5	9.0	341	3	US-08-928-100-2	Sequence 2, Appli
5	185.5	9.0	341	4	US-09-492-581-2	Sequence 2, Appli
6	185.5	9.0	341	4	US-09-425-666-2	Sequence 2, Appli
7	169.5	8.2	409	2	US-08-743-130A-39	Sequence 39, Appl
8	167.5	8.1	409	2	US-08-743-130A-2	Sequence 2, Appli
9	152	7.3	344	4	US-09-198-452A-857	Sequence 857, App
10	137	6.6	388	2	US-08-705-868-4	Sequence 4, Appli
11	137	6.6	388	3	US-09-123-615-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: February 20, 2004, 12:46:42 ; Search time 30.0364 Seconds
(without alignments)
2732.616 Million cell updates/sec

Title: US-10-080-839-7
Perfect score: 2071
Sequence: 1 MSAKGIDYDKLIVREFGSSKI.....KLSFDFQKLAAALEHHHHHH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2071	100.0	392	10	US-09-813-718-16	Sequence 16, Appl
2	2071	100.0	392	12	US-10-240-532-16 ^(new)	Sequence 16, Appl
3	2066	99.8	415	10	US-09-813-718-14	Sequence 14, Appl
4	2066	99.8	415	12	US-10-240-532-14	Sequence 14, Appl
5	2066	99.8	437	10	US-09-813-718-12	Sequence 12, Appl
6	2066	99.8	437	12	US-10-240-532-12	Sequence 12, Appl
7	2066	99.8	484	10	US-09-813-718-10	Sequence 10, Appl
8	2066	99.8	484	12	US-10-240-532-10	Sequence 10, Appl
9	1988	96.0	471	12	US-10-295-027-1234	Sequence 1234, Ap
10	1988	96.0	471	15	US-10-126-467B-2	Sequence 2, Appli
11	1973	95.3	471	11	US-09-919-039-163	Sequence 163, App
12	1973	95.3	471	12	US-10-247-671-166	Sequence 166, App
13	1973	95.3	475	9	US-09-925-302-558	Sequence 558, App
14	1853	89.5	475	12	US-10-205-219-65	Sequence 65, Appl
15	1177.5	56.9	424	12	US-10-032-585-7632	Sequence 7632, Ap
16	1119.5	54.1	433	15	US-10-128-714-8545	Sequence 8545, Ap
17	1099	53.1	456	12	US-10-320-797-3204	Sequence 3204, Ap
18	831	40.1	173	9	US-09-925-302-855	Sequence 855, App
19	409	19.7	179	15	US-10-128-714-3545	Sequence 3545, Ap
20	228	11.0	286	12	US-09-930-512-32	Sequence 32, Appl
21	200	9.7	85	10	US-09-813-718-45	Sequence 45, Appl
22	200	9.7	85	12	US-10-240-532-45	Sequence 45, Appl
23	191	9.2	85	10	US-09-813-718-46	Sequence 46, Appl
24	191	9.2	85	12	US-10-240-532-46	Sequence 46, Appl
25	187	9.0	85	10	US-09-813-718-48	Sequence 48, Appl
26	187	9.0	85	12	US-10-240-532-48	Sequence 48, Appl
27	185.5	9.0	341	9	US-09-815-242-13444	Sequence 13444, A
28	178	8.6	85	10	US-09-813-718-47	Sequence 47, Appl
29	178	8.6	85	12	US-10-240-532-47	Sequence 47, Appl
30	173	8.4	372	10	US-09-813-718-8	Sequence 8, Appli
31	173	8.4	372	12	US-10-240-532-8	Sequence 8, Appli
32	171.5	8.3	372	10	US-09-813-718-4	Sequence 4, Appli
33	171.5	8.3	372	12	US-10-240-532-4	Sequence 4, Appli
34	169.5	8.2	409	12	US-10-032-585-7335	Sequence 7335, Ap
35	152	7.3	344	12	US-10-289-762-857	Sequence 857, App
36	147	7.1	385	15	US-10-128-714-3379	Sequence 3379, Ap
37	146.5	7.1	391	15	US-10-128-714-8379	Sequence 8379, Ap
38	146	7.0	339	9	US-09-815-242-11422	Sequence 11422, A
39	142.5	6.9	337	15	US-10-156-761-10954	Sequence 10954, A
40	141.5	6.8	399	12	US-10-320-797-3147	Sequence 3147, Ap
41	137	6.6	536	10	US-09-813-718-2	Sequence 2, Appli
42	137	6.6	536	12	US-10-240-532-2	Sequence 2, Appli
43	128	6.2	334	9	US-09-815-242-11070	Sequence 11070, A
44	119	5.7	415	12	US-09-930-512-4	Sequence 4, Appli
45	113.5	5.5	423	9	US-09-815-242-10678	Sequence 10678, A

ALIGNMENTS

RESULT 1

US-09-813-718-16

OM protein - protein search, using sw model

Run on: February 20, 2004, 12:42:31 ; Search time 16.8 Seconds
 (without alignments)
 2243.936 Million cell updates/sec

Title: US-10-080-839-7
 Perfect score: 2071
 Sequence: 1 MSAKGIDYDKLIVRFGSSKI.....KLSFDFQKLAAALEHHHHHHH 392

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_76:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1973	95.3	471	1	A41706	tryptophan-tRNA li	
2	1927.5	93.1	475	1	YWBO	tryptophan-tRNA li	
3	1864	90.0	475	1	YWRBPR	tryptophan-tRNA li	
4	1853	89.5	481	2	S50053	tryptophan-tRNA li	
5	1186	57.3	395	2	S58157	hypothetical prote	
6	1138.5	55.0	432	2	S51901	tryptophan-tRNA li	
7	891.5	43.0	386	2	C90190	tryptophanyl-tRNA	
8	786.5	38.0	385	2	C75020	tryptophanyl-tRNA	
9	626.5	30.3	301	2	G71206	tryptophan-tRNA li	
10	526	25.4	380	2	G84373	tryptophanyl-tRNA	
11	406.5	19.6	370	2	F64476	tryptophan-tRNA li	
12	382.5	18.5	364	2	E69131	tryptophan-tRNA li	
13	370	17.9	134	2	T43806	tryptophan-tRNA li	

OM protein - protein search, using sw model

Run on: February 20, 2004, 12:38:51 ; Search time 10.1818 Seconds
(without alignments)
1810.528 Million cell updates/sec

Title: US-10-080-839-7
Perfect score: 2071
Sequence: 1 MSAKGIDYDKLIVRFGSSKI.....KLSFDFQKLAAALEHHHHHHH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1973	95.3	471	1	SYW_HUMAN	P23381 homo sapien
2	1927.5	93.1	475	1	SYW_BOVIN	P17248 bos taurus
3	1879	90.7	475	1	SYW_RABIT	P23612 oryctolagus
4	1853	89.5	481	1	SYW_MOUSE	P32921 mus musculu
5	1186	57.3	395	1	SYW_SCHPO	Q09692 schizosacch
6	1138.5	55.0	432	1	SYWC_YEAST	Q12109 saccharomyc
7	895.5	43.2	381	1	SYW_SULTO	Q976m1 sulfolobus
8	891.5	43.0	380	1	SYW_SULSO	Q97zx0 sulfolobus
9	809	39.1	385	1	SYW_PYRFU	Q8u453 pyrococcus
10	786.5	38.0	385	1	SYW_PYRAB	Q9uy11 pyrococcus
11	782	37.8	386	1	SYW_PYRHO	O59584 pyrococcus
12	717.5	34.6	375	1	SYW_PYRAE	Q8ztu5 pyrobaculum
13	526	25.4	380	1	SYW_HALN1	Q9hn66 halobacteri
14	434.5	21.0	374	1	SYW_METKA	Q8tyf7 methanopyru
15	406.5	19.6	370	1	SYW_METJA	Q58810 methanococc
16	382.5	18.5	364	1	SYW_METTH	O26352 methanobact
17	370	17.9	134	1	SYW_ENCCU	O96771 encephalito